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Chimeric binding peptide library screening method

The present invention relates generally to methods for screening nucleotide libraries for sequences that encode peptides of interest.

Isolating an unknown gene which encodes a desired peptide from a recombinant DNA library can be a difficult task. The use of hybridisation probes may facilitate the process, but their use is generally dependent on knowing at least a portion of the sequence of the gene which encodes the protein. When the sequence is not known, DNA libraries can be expressed in an expression vector, and antibodies have been used to screen for plagues or colonies displaying the desired protein antigen. This procedure has been useful in screening small libraries, but rarely occurring sequences which are represented in less than about 1 in 105 clones (as is the case with rarely occurring cDNA molecules or synthetic peptides) can be easily missed, making screening libraries larger than 106 clones at 21 best laborious and difficult. Methods designed to address the isolation of rarely occurring sequences by screening libraries of 106 clones have been developed and include phage display methods and LacI fusion phage

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display, discussed in more detail below.
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                              Members of DNA libraries which
      Phage display methods.
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      are fused to the N-terminal end of filamentous
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      bacteriophage pIII and pVIII coat proteins have been
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      expressed from an expression vector resulting in the
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      display of foreign peptides on the surface of the phage
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      particle with the DNA encoding the fusion protein
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      packaged in the phage particle (Smith G. P., 1985,
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      Science 228: 1315-1317). The expression vector can be
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      the bacteriophage genome itself, or a phagemid vector,
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      into which a bacteriophage coat protein has been
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     cloned. In the latter case, the host bacterium,
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      containing the phagemid vector, must be co-infected
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      with autonomously replicating bacteriophage, termed
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      helper phage, to provide the full complement of
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      proteins necessary to produce mature phage particles.
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      The helper phage normally has a genetic defect in the
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      origin of replication which results in the preferential
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      packaging of the phagemid genome. Expression of the
20
      fusion protein following helper phage infection, allows
21
      incorporation of both fusion protein and wild type coat
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      protein into the phage particle during assembly.
23
      Libraries of fusion proteins incorporated into phage,
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      can then be selected for binding members against
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      targets of interest (ligands). Bound phage can then be
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      allowed to reinfect Escherichia coli (E. coli) bacteria
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      and then amplified and the selection repeated,
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      resulting in the enrichment of binding members
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      (Parmley, S. F., & Smith, G. P. 1988., Gene 73: 305-
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      318; Barrett R. W. et al., 1992, Analytical
      Biochemistry 204: 357-364 Williamson et al., Proc.
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      Natl. Acad. Sci. USA, 90: 4141-4145; Marks et al.,
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      1991, J. Mol. Biol. 222: 581-597).
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Several publications describe this method. For example,

| , T | US Patent NO 5,403,484 describes production of a |
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| 2 | chimeric protein formed from the viral coat protein and |
| 3 | the peptide of interest. In this method at least a |
| 4 | functional portion of a viral coat protein is required |
| 5 | to cause display of the chimeric protein or a processed |
| 6 | form thereof on the outer surface of the virus. In |
| 7 | addition, US Patent No 5,571,698 describes a method for |
| 8 | obtaining a nucleic acid encoding a binding protein, a |
| 9 | key component of which comprises preparing a population |
| 10 | of amplifiable genetic packages which have a |
| 11 | genetically determined outer surface protein, to cause |
| 12 | the display of the potential binding domain on the |
| 13 | outer surface of the genetic package. The genetic |
| 14 | packages are selected from the group consisting of |
| 15 | cells, spores and viruses. For example when the |
| 16 | genetic package is a bacterial cell, the outer surface |
| 17 | transport signal is derived from a bacterial outer |
| 18 | surface protein, and when the genetic package is a |
| 19 | filamentous bacteriophage, the outer surface transport |
| 20 | signal is provided by the gene pIII (minor coat |
| 21 | protein) or pVIII (major coat protein) of the |
| 22 | filamentous phage. |

WO-A-92/01047 and WO-A-92/20791 describe methods for producing multimeric specific binding pairs, by expressing a first polypeptide chain fused to a viral coat protein, such as the gene pIII protein, of a secreted replicable genetic display package (RGDP) which displays a polypeptide at the surface of the package, and expressing a second polypeptide chain of the multimer, and allowing the two chains to come together as part of the RGDP.

LacI fusion plasmid display. This method is based on the DNA binding ability of the lac repressor. Libraries of random peptides are fused to the lacI repressor

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protein, normally to the C-terminal end, through expression from a plasmid vector carrying the fusion gene. Linkage of the LacI-peptide fusion to its encoding DNA occurs via the lacO sequences on the plasmid, forming a stable peptide-LacI-peptide complex. These complexes are released from their host bacteria by cell lysis, and peptides of interest isolated by affinity purification on an immobilised target. The plasmids thus isolated can then be reintroduced into E. coli by electroporation to amplify the selected population for additional rounds of screening (Cull, M. G. et al. 1992. Proc. Natl. Acad. Sci. U.S.A. 89:1865-1869).

US Patent No 5498530 describes a method for constructing a library of random peptides fused to a DNA binding protein in appropriate host cells and culturing the host cells under conditions suitable for expression of the fusion proteins intra-cellularly, in the cytoplasm of the host cells. This method also teaches that the random peptide is located at the carboxy terminus of the fusion protein and that the fusion protein-DNA complex is released from the host cell by cell lysis. No method is described for the protection of the DNA from degradation once released from the lysed cell. Several DNA binding proteins are claimed but no examples are shown except lacI.

There remains a need for methods of constructing peptide libraries in addition to the methods described above. For instance, the above methods do not permit production of secreted peptides with a free carboxy terminus. The present invention describes an alternative method for isolating peptides of interest from libraries and has significant advantages over the prior art methods.

In general terms, the present invention provides a method for screening a nucleotide library (usually a DNA library) for a nucleotide sequence which encodes a target peptide of interest. The method involves physically linking each peptide to a polynucleotide including the specific nucleotide sequence encoding that peptide. Linkage of a peptide to its encoding nucleotide sequence is achieved via linkage of the peptide to a nucleotide binding domain. A bifunctional chimeric protein with a nucleotide binding domain and a library member or target peptide (preferably with a function of interest) is thus obtained. The peptide of interest is bound to the polynucleotide encoding that peptide via the nucleotide binding domain of the chimeric protein.

The polynucleotide-chimeric protein complex is then incorporated within a peptide display carrier package (PDCP), protecting the polynucleotide from subsequent degradation, while displaying the target peptide portion on the outer surface of the peptide display carrier package (PDCP).

Thus, in one aspect, the present invention provides a peptide display carrier package (PDCP), said package comprising a polynucleotide-chimeric protein complex wherein the chimeric protein has a nucleotide binding portion and a target peptide portion, wherein said polynucleotide comprises a nucleotide sequence motif which is specifically bound by said nucleotide binding portion, and wherein at least the chimeric protein encoding portion of the polynucleotide not bound by the nucleotide binding portion of the chimeric protein is protected.

In one embodiment the polynucleotide is protected by a

protein which binds non-specifically to naked Examples include viral coat proteins, polynucleotide. many of which are well-known in the art. chosen viral coat protein requires an initiation sequence to commence general binding to the polynucleotide, this will be provided on the polynucleotide at appropriate location(s). A preferred coat protein is coat protein from a bacteriophage,

especially M13.

Generally, the nucleic binding portion of the chimeric protein is selected for its specificity for the nucleotide sequence motif present in the recombinant polynucleotide encoding the chimeric protein.

optionally, the nucleotide sequence motif may be an integral part of the protein encoding region of the polynucleotide. Alternatively, and more usually, the motif may be present in a non-coding region of the polynucleotide. For the purposes of this invention, all that is required is for the motif to be located on the polynucleotide such that the nucleotide binding portion of the chimeric protein is able to recognise and bind to it. Desirably the polynucleotide-chimeric protein complex has a dissociation constant of at least one hour.

Optionally, the recombinant polynucleotide may comprise two or more nucleotide sequence motifs, each of which will be bound by a chimeric protein molecule. Preferably, the motifs are positioned along the length of the polynucleotide to avoid steric hindrance between the bound chimeric proteins.

Preferably, the nucleotide sequence motif is not affected by the presence of additional nucleotide

sequence (e.g. encoding sequence) at its 5' and/or 3' ends. Thus the chimeric fusion protein may include a target peptide portion at its N terminal end, at its C terminal end or may include two target peptide portions (which may be the same or different) at each end of the nucleotide binding portion, ie at both the N and C terminal ends of the chimeric protein. For example one target peptide may be an antibody of known specificity and the other peptide may be a peptide of potential interest.

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Desirably the target peptide portion of the chimeric protein is displayed externally on the peptide display carrier package, and is thus available for detection, reaction and/or binding.

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In more detail the PDCP may be composed two distinct elements:

a. A polynucleotide-chimeric protein complex. This links the displayed target peptide portion to the polynucleotide encoding that peptide portion through a specific polynucleotide binding portion. The nucleotide sequence encoding the chimeric protein, and the specific nucleotide sequence motif recognised by the nucleotide binding portion of the chimeric protein must be present on a segment of polynucleotide which can be incorporated into the PDCP; and b. A protective coat. This may be supplied by a replicable carrier or helper package capable of independent existence. Alternatively, a coat protein could be encoded by the recombinant polynucleotide of the invention. The protective coat for the polynucleotide-chimeric protein complex may be composed of a biological material such as protein or lipid, but the protective coat

is not required for linking the target peptide to the polynucleotide encoding that peptide. The protective coat must allow the display of the target peptide portion of the chimeric protein on its outer surface. The carrier or helper package may also provide the mechanism for releasing the intact PDCP from host cells when so required. By way of example, when a bacteriophage is the replicable carrier package, a protein coat of the bacteriophage surrounds the polynucleotide—chimeric protein complex to form the PDCP, which is then extruded from the host bacterial cell.

The invention described herein demonstrates that peptides fused to a nucleotide binding domain can be displayed externally, even through a bacteriophage carrier package protein coat, while still bound to the polynucleotide encoding the displayed peptide.

The present invention also provides a recombinant polynucleotide comprising a nucleotide sequence encoding a chimeric protein having a nucleotide binding portion operably linked to a target peptide portion, wherein said polynucleotide includes a specific nucleotide sequence motif which is bound by the nucleotide binding portion of said chimeric protein and further encoding a non-sequence-specific nucleotide binding protein.

Desirably, the recombinant polynucleotide is a recombinant expression system, able to express the chimeric protein when placed in a suitable environment, for example a compatible host cell. After its expression, the chimeric protein binds to the specific nucleotide sequence (motif) present in the polynucleotide comprising the nucleotide sequence

1 encoding the chimeric protein.

Optionally there may be a linker sequence located between the nucleotide sequence encoding the nucleotide binding portion and the polynucleotide inserted into the restriction enzyme site of the construct.

Desirably the nucleotide binding portion is a DNA binding domain of an oestrogen or progesterone receptor, or a functional equivalent thereof. Examples of sequences encoding such nucleotide binding portions are set out in SEQ ID Nos 11 and 13.

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The term "expression system" is used herein to refer to a genetic sequence which includes a protein-encoding region and is operably linked to all of the genetic signals necessary to achieve expression of that region. Optionally, the expression system may also include regulatory elements, such as a promoter or enhancer to increase transcription and/or translation of the protein encoding region or to provide control over expression. The regulatory elements may be located upstream or downstream of the protein encoding region or within the protein encoding region itself. Where two or more distinct protein encoding regions are present these may use common regulatory element(s) or have separate regulatory element(s).

Generally, the recombinant polynucleotide described above will be DNA. Where the expression system is based upon an M13 vector, usually the polynucleotide binding portion of the expressed chimeric portion will be single-stranded DNA. However, other vector systems may be used and the nucleotide binding portion may be selected to bind preferentially to double-stranded DNA or to double or single-stranded RNA, as convenient.

Additionally the present invention provides a vector containing such a recombinant expression system and host cells transformed with such a recombinant expression system (optionally in the form of a vector).

Whilst the recombinant polynucleotide described above forms an important part of the present invention, we are also concerned with the ability to screen large (e.g. of at least 10⁵ members, for example 10⁶ or even 10⁷ members) libraries of genetic material. One of the prime considerations therefore is the provision of a recombinant genetic construct into which each member of said library can individually be incorporated to form the recombinant polynucleotide described above and to express the chimeric protein thereby encoded (the target peptide of which is encoded by the nucleotide library member incorporated into the construct).

Thus viewed in a further aspect the present invention provides a genetic construct or set of genetic constructs comprising a polynucleotide having a sequence which includes:

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- i) a sequence encoding a nucleotide binding portion able to recognise and bind to a specific sequence motif;
- ii) the sequence motif recognised and bound by the nucleotide binding portion encoded by (i);

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- iii) a restriction enzyme site which permits insertion of a polynucleotide, said site being designed to operably link said polynucleotide to the sequence encoding the nucleotide binding portion so that expression of the operably linked polynucleotide sequences yields a chimeric protein; and
- iv) a sequence encoding a nucleotide binding protein
 which binds non-specifically to naked

polynucleotide.

Optionally there may be a linker sequence located between the nucleotide sequence encoding the nucleotide binding portion and the sequence of the polynucleotide from the library inserted into the restriction enzyme site of the construct.

Desirably the nucleotide binding portion is a DNA binding domain of an oestrogen or progesterone receptor, or a functional equivalent thereof. Examples of sequences encoding such nucleotide binding portions are set out in SEQ ID Nos 11 and 13.

Suitable genetic constructs according to the invention include pDM12, pDM14 and pDM16, deposited at NCIMB on 28 August 1998 under Nos NCIMB 40970, NCIMB 40971 and NCIMB 40972 respectively.

It is envisaged that a conventionally produced genetic library may be exposed to the genetic construct(s) described above. Thus, each individual member of the genetic library will be separately incorporated into the genetic construct and the library will be present in the form of a library of recombinant polynucleotides (as described above), usually in the form of vectors, each recombinant polynucleotide including as library member.

Thus, in a further aspect, the present invention provides a library of recombinant polynucleotides (as defined above) wherein each polynucleotide includes a polynucleotide obtained from a genetic library and which encodes the target peptide portion of the chimeric protein expressed by the recombinant polynucleotide.

Optionally, the chimeric protein may further include a linker sequence located between the nucleotide binding portion and the target peptide portion. The linker sequence will reduce steric interference between the two portions of the protein. Desirably the linker sequence exhibits a degree of flexibility.

 Also disclosed are methods for constructing and screening libraries of PDCP particles, displaying many different peptides, allowing the isolation and identification of particular peptides by means of affinity techniques relying on the binding activity of the peptide of interest. The resulting polynucleotide sequences can therefore be more readily identified, recloned and expressed.

A method of constructing a genetic library, said method comprising:

a) constructing multiple copies of a recombinant vector comprising a polynucleotide sequence which encodes a nucleotide binding portion able to recognise and bind to a specific sequence motif (and optionally also including the specific sequence motif);

b) operably linking each said vector to a polynucleotide encoding a target polypeptide, such that expression of said operably linked vector results in expression of a chimeric protein comprising said target peptide and said nucleotide binding portions; wherein said multiple copies of said operably linked vectors collectively express a library of target peptide portions;

c) transforming host cells with the vectors of step

b):

| - | | |
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| 2 | | |
| 3 | d) | culturing the host cells of step c) under |
| 4 | | conditions suitable for expression of said |
| 5 | | chimeric protein; |
| 6 | | |
| 7 | e) | providing a recombinant polynucleotide comprising |
| 8 | | the nucleotide sequence motif specifically |
| 9 | | recognised by the nucleotide binding portion and |
| 10 | | exposing this polynucleotide to the chimeric |
| 11 | | protein of step d) to yield a polynucleotide- |
| 12 | | chimeric protein complex; and |

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causing production of a non-sequence-specific f) moiety able to bind to the non-protected portion of the polynucleotide encoding the chimeric protein to form a peptide display carrier package.

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The present invention further provides a method of screening a genetic library, said method comprising:

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exposing the polynucleotide members of said library to multiple copies of a genetic construct comprising a nucleotide sequence encoding a nucleotide binding portion able to recognise and bind to a specific sequence motif, under conditions suitable for the polynucleotides of said library each to be individually ligated into one copy of said genetic construct, to create a library of recombinant polynucleotides;

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exposing said recombinant polynucleotides to a 32 -b) population of host cells, under conditions 33 suitable for transformation of said host cells by 34 said recombinant polynucleotides; 35

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| 1 | c) selecting for transformed host cells; |
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| 2 | |
| 3 | d) exposing said transformed host cells to conditions |
| 4 | suitable for expression of said recombinant |
| 5 | polynucleotide to yield a chimeric protein; and |
| 6 | |
| 7 | e) providing a recombinant polynucleotide comprising |
| 8 | the nucleotide sequence motif specifically |
| 9 | recognised by the nucleotide binding portion and |
| 10 | exposing this polynucleotide to the chimeric |
| 11 | protein of step d) to yield a polynucleotide- |
| 12 | chimeric protein complex; |
| 13 | |
| 14 | f) protecting any exposed portions of the |
| 15 | polynucleotide in the complex of step e) to form a |
| 16 | peptide display carrier package; and |
| 17 | and the state of t |
| 18 | g) screening said peptide display carrier package to |
| 19 | select only those packages displaying a target |
| 20 | peptide portion having the characteristics |
| 21 | required. |
| 22 | |
| 23 | Desirably in step a) the genetic construct is pDM12, |
| 24 | pDM14 or pDM16. |
| 2.5 | the design of the property of the second section of the se |
| 26 | Desirably in step f) the peptide display package |
| 27 | carrier is extruded from the transformed host cell |
| 28 | without lysis of the host cell. |
| 29 | |
| 3.0 | Generally the transformed host cells will be plated out |
| 31 | or otherwise divided into single colonies following |
| 32 | transformation and prior to expression of the chimeric |
| 33 | protein. |
| 34 | |
| 35 | The screening step g) described above may look for a |

particular target peptide either on the basis of

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function (e.g. enzymic activity) or structure (e.g. binding to a specific antibody). Once the peptide display carrier package is observed to include a target peptide with the desired characteristics, the polynucleotide portion thereof (which of course encodes the chimeric protein itself) can be amplified, cloned and otherwise manipulated using standard genetic engineering techniques.

The current invention differs from the prior art teaching of the previous disclosures US Patent No 5,403,484 and US Patent No 5,571,698, as the invention does not require outer surface transport signals, or functional portions of viral coat proteins, to enable the display of chimeric binding proteins on the outer surface of the viral particle or genetic package.

The current invention also differs from the teaching of WO-A-92/01047 and WO-A-92/20791, as no component of a secreted replicable genetic display package, or viral coat protein is required, to enable display of the target peptide on the outer surface of the viral particle.

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The current invention differs from the teaching of US.
Patent No 5498530, as it enables the display of chimeric proteins, linked to the polynucleotide encoding the chimeric protein, extra-cellularly, not in the cytoplasm of a host cell. In the current invention the chimeric proteins are presented on the outer surface of a peptide display carrier package (PDCP) which protects the DNA encoding the chimeric protein, and does not require cell lysis to obtain access to the chimeric protein-DNA complex. Finally, the current invention does not rely upon the lacI DNA binding protein to form the chimeric protein-DNA complex.

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In one embodiment of the invention, the nucleotide binding portion of the chimeric protein comprises a DNA binding domain from one or more of the nuclear steroid receptor family of proteins, or a functional equivalent of such a domain. Particular examples include (but are not limited to) a DNA binding domain of the oestrogen receptor or the progesterone receptor, or functional equivalents thereof. These domains can recognise specific DNA sequences, termed hormone response elements (HRE), which can be bound as both double and single-stranded DNA. The DNA binding domain of such nuclear steroid receptor proteins is preferred.

The oestrogen receptor is especially referred to below by way of example, for convenience since:

(a) The oestrogen receptor is a large multifunctional polypeptide of 595 amino acids which functions in the cytoplasm and nucleus of eukaryotic cells (Green et al., 1986, Science 231: 1150-1154). A minimal high affinity DNA binding domain (DBD) has been defined between amino acids 176 and 282 (Mader et al., 1993, Nucleic Acids Res. 21: 1125-1132). The functioning of this domain (i.e. DNA binding) is not inhibited by the presence of non-DNA binding domains at both the N and C terminal ends of this domain, in the full length protein.

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(b) The oestrogen receptor DNA binding domain fragment (amino acids 176-282) has been expressed in *E. coli* and shown to bind to the specific double stranded DNA oestrogen receptor target HRE nucleotide sequence, as a dimer with a similar affinity (0.5nM) to the parent molecule (Murdoch et al. 1990, Biochemistry 29: 8377-8385; Mader-et al., 1993, Nucleic Acids Research-21: 1125-1132). DBD dimerization on the surface of the PDCP should result in two peptides displayed per particle.

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1 This bivalent display can aid in the isolation of low affinity peptides and peptides that are required to 2 form a bivalent conformation in order to bind to a particular target, or activate a target receptor. The oestrogen receptor is capable of binding/to its 38 base 5 pair target HRE sequence, consensus segmence:

- 1) 5'-TCAGGTCAGAGTGACCTGAGCTAAAATAXCACATTCAG-3' ("minus strand") SEQ ID No 1, and
- 3'-AGTCCAGTCTCACTGGACTCGATTTTATTGTGTAAGTC-5' 2) ("plus strand") SEQ ID No 2

with high affinity and specificity, under the salt and pH conditions normally required for selection of binding peptides. Moreover, binding affinity is increased 60-fold for the single-stranded coding, or "plus", strand (i.e. SEQ/ID No 2) of the HRE nucleotide sequence over the double stranded form of the specific target nucleotide sequénce (Peale et al. 1988, Proc. . . Natl. Acad. Sci. USA \$5: 1038-1042; Lannigan & Notides, 1989, Proc. Natl. Acad. Sci. USA 86: 863-867).

In an embodiment of the invention where the DNA binding component of the/peptide display carrier package is the oestrogen receptor, the nucleotide (DNA) binding portion contains a minimum sequence of amino acids 176-282 of the oestrogen receptor protein. In addition, the consensus ogstrogen receptor target HRE sequence is cloned in such a way that if single stranded DNA can be produced then the coding, or "plus", strand of the oestrogen receptor HRE nucleotide sequence is incorporated into single-stranded DNA. An example of a vector/suitable for this purpose is pUC119 (see Viera et al√, Methods in Enzymology, Vol 153, pages 3-11, 1987)/.

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In a preferred embodiment of the invention a peptide 1 display carrier package (PDCP) can be assembled when a 2 bacterial host cell is transformed with a bacteriophage 3 vector, which vector comprises a recombinant 4 5 polynucleotide as described above. The expression vector will also comprise the specific nucleotide motif 6 that can be bound by the nucleotide binding portion of 7 the chimeric protein. Expression of recombinant 8 polynucleotide results in the production of the 9 chimeric protein which comprises the target peptide and 10 the nucleotide binding portion. The host cellais grown 11 under conditions suitable for chimeric protein 12 expression and assembly of the bacteriophage particles, 13 and the association of the chimeric protein with the 14 specific nucleotide sequence in the expression vector. 15

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In this embodiment, since the vector is a bacteriophage, which replicates to produce a single-stranded DNA, the nucleotide binding portion preferably has an affinity for single-stranded DNA. Incorporation of the vector single-stranded DNA-chimeric protein complex into bacteriophage particles results in the assembly of the peptide display carrier package (PDCP), and display of the target peptide on the outer surface of the PDCP.

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In this embodiment both of the required elements for producing peptide display carrier packages are contained on the same vector. Incorporation of the DNA-chimeric protein complex into a peptide display carrier package (PDCP) is preferred as DNA degradation is prevented, large numbers of PDCPs are produced per host cell, and the PDCPs are easily separated from the host cell without recourse to cell lysis.

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In a more preferred embodiment, the vector of the is a

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phagemid vector (for example pUC119) where expression of the chimeric protein is controlled by an inducible promoter. In this embodiment the PDCP can only be assembled following infection of the host cell with both phagemid vector and helper phage. The transfected host cell is then cultivated under conditions suitable for chimeric protein expression and assembly of the bacteriophage particles.

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In this embodiment the elements of the PDCP are provided by two separate vectors. The phagemid derived PDCP is superior to phagemid derived display packages disclosed in WO-A-92/01047 where a proportion of packages displaying bacteriophage coat protein fusion proteins will contain the helper phage DNA, not the fusion protein DNA sequence. In the current invention, a PDCP can display the chimeric fusion protein only when the package contains the specific nucleotide motif recognised by the nucleotide binding portion. In most embodiments this sequence will be present on the same DNA segment that encodes the fusion protein. In addition, the prior art acknowledges that when mutant and wild type proteins are co-expressed in the same bacterial cell, the wild type protein is produced preferentially. Thus, when the wild type helper phage, phage display system of WO-A-92/01047 is used, both wild type gene pIII and target peptide-gene pIII chimeric proteins are produced in the same cell. The result of this is that the wild type gene pIII protein is preferentially packaged into bacteriophage particles, over the chimeric protein. In the current invention, there is no competition with wild type

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Desirably the target peptide is displayed in a location exposed to the external environment of the PDCP, after

bacteriophage coat proteins for packaging.

the PDCP particle has been released from the host cell without recourse to cell lysis. The target peptide is then accessible for binding to its ligand. Thus, the target peptide may be located at or near the N-terminus or the C-terminus of a nucleotide binding domain, for example the DNA binding domain of the oestrogen receptor.

The present invention also provides a method for screening a DNA library expressing one or more polypeptide chains that are processed, folded and assembled in the periplasmic space to achieve biological activity. The PDCP may be assembled by the following steps:

(a) Construction of N- or C-terminal DBD chimeric protein fusions in a phagemid vector.

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- (i) When the target peptide is located at the N-terminus of the nucleotide binding portion, a library of DNA sequences each encoding a potential target peptide is cloned into an appropriate location of an expression vector (i.e. behind an appropriate promoter and translation sequences and a sequence encoding a signal peptide leader directing transport of the downstream fusion protein to the periplasmic space) and upstream of the sequence encoding the nucleotide binding portion. In a preferred embodiment the DNA sequence(s) of interest may be joined, by a region of DNA encoding a flexible amino acid linker, to the 5'-end of an oestrogen receptor DBD.
- (ii) Alternatively, when the target peptide is located at the C-terminus of the nucleotide binding domain, a library of DNA sequences each encoding a potential target peptide is cloned into the expression vector so that the nucleotide sequence coding for the nucleotide binding portion is upstream of the cloned

DNA target peptide encoding sequences, said nucleotide binding portion being positioned behind an appropriate promoter and translation sequences and a sequence encoding a signal peptide leader directing transport of the downstream fusion protein to the periplasmic space. In a preferred embodiment, DNA sequence(s) of interest may be joined, by a region of DNA encoding a flexible amino acid linker oestrogen receptor DBD DNA sequence.

Located on the expression vector is the specific HRE nucleotide sequence recognised, and bound, by the oestrogen receptor DBD. In order to vary the number of chimeric proteins displayed on each PDCP particle, this sequence can be present as one or more copies in the vector.

(b) Incorporation into the PDCP. Non-lytic helper bacteriophage infects host cells containing the expression vector. Preferred types of bacteriophage include the filamentous phage fd, fl and M13. In a more preferred embodiment the bacteriophage may be M13K07.

The protein(s) of interest are expressed and transported to the periplasmic space, and the properly assembled proteins are incorporated into the PDCP particle by virtue of the high affinity interaction of the DBD with the specific target nucleotide sequence present on the phagemid vector DNA which is naturally packaged into phage particles in a single-stranded form. The high affinity interaction between the DBD protein and its specific target nucleotide sequence prevents displacement by bacteriophage coat proteins resulting in the incorporation of the protein(s) of interest onto the surface of the PDCP as it is extruded from the cell.

(c) Selection of the peptide of interest. Particles which display the peptide of interest are then selected from the culture by affinity enrichment techniques. This is accomplished by means of a ligand specific for the protein of interest, such as an antigen if the protein of interest is an antibody. The ligand may be presented on a solid surface such as the surface of an ELISA plate, or in solution. Repeating the affinity selection procedure provides an enrichment of clones encoding the desired sequences, which may then be isolated for sequencing, further cloning and/or expression.

Numerous types of libraries of peptides fused to the DBD can be screened under this embodiment including:

(i) Random peptide sequences encoded by synthetic DNA of variable length.

(ii) Single-chain Fv antibody fragments. These consist of the antibody heavy and light chain variable region domains joined by a flexible linker peptide to create a single-chain antigen binding molecule.

(iii) Random fragments of naturally occurring proteins isolated from a cell population containing an activity of interest.

In another embodiment the invention concerns methods for screening a DNA library whose members require more than one chain for activity, as required by, for example, antibody Fab fragments for ligand binding. In this embodiment heavy or light chain antibody DNA is joined to a nucleotide sequence encoding a DNA binding domain of, for example, the oestrogen receptor in a

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phagemid vector. Typically the antibody DNA library sequences for either the heavy (VH and CH1) or light chain (VL and CL) genes are inserted in the 5' region of the oestrogen receptor DBD DNA, behind an appropriate promoter and translation sequences and a sequence encoding a signal peptide leader directing transport of the downstream fusion protein to the periplasmic space.

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 Thus, a DBD fused to a DNA library member-encoded protein is produced and assembled in to the viral particle after infection with bacteriophage. The second and any subsequent chain(s) are expressed separately either:

(a) from the same phagemid vector containing the DBD and the first polypeptide fusion protein, or

(b) from a separate region of DNA which may be present in the host cell nucleus, or on a plasmid, phagemid or bacteriophage expression vector that can co-exist, in the same host cell, with the first expression vector, so as to be transported to the periplasm where they assemble with the first chain that is fused to the DBD protein as it exits the cell. Peptide display carrier packages (PDCP) which encode the protein of interest can then be selected by means of a ligand specific for the protein.

In yet another embodiment, the invention concerns
screening libraries of bi-functional peptide display
carrier packages where two or more activities of
interest are displayed on each PDCP. In this
embodiment, a first DNA library sequence(s) is inserted
next to a first DNA binding domain (DBD) DNA sequence,

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1 for example the oestrogen receptor DBD, in an 2 appropriate vector, behind an appropriate promoter and 3 translation sequences and a sequence encoding a signal 4 peptide leader directing transport of this first chimeric protein to the periplasmic space. A second 5 chimeric protein is also produced from the same, or 6 separate, vector by inserting a second DNA library 7 sequence(s) next to a second DBD DNA sequence which is 8 different from the first DBD DNA sequence, for example 9 the progesterone receptor DBD; behind an appropriate 10 promoter, and translation sequences and a sequence 11 encoding a signal peptide leader. The first, or only, 12 13 vector contains the specific HRE nucleotide sequences 14 for both oestrogen and progesterone receptors. 15 Expression of the two chimeric proteins, results in a PDCP with two different chimeric proteins displayed. As 16 an example, one chimeric protein could possess a 17 binding activity for a particular ligand of interest, 18 while the second chimeric protein could possess an 19 enzymatic activity wBinding by the PDCR: to the whigand) 20 21 of the first chimeric protein could then be detected by 22 subsequent incubation with an appropriate substrate for the second chimeric protein. In an alternative 23 24 embodiment a bi-functional PDCP may be created using a 25 single DBD, by acloning one peptide sat the d5 -end of the 26 DBD, and a second peptide at the 3'-end of the DBD. 27 Expression of this single bi-functional chimeric protein results in a PDCP with two different and a 28 29 activities.

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We have investigated the possibility of screening
libraries of peptides, fused to a DNA binding domain
and displayed on the surface of a display package, for
particular peptides with a biological activity of
interest and recovering the DNA encoding that activity.
Surprisingly, by manipulating the oestrogen receptor

DNA binding domain in conjunction with M13
bacteriophage we have been able to construct novel
particles which display large biologically functional
molecules, that allows enrichment of particles with the
desired specificity.

The invention described herein provides a significant breakthrough in DNA library screening technology.

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The invention will now be further described by reference to the non-limiting examples and figures below.

Description of Figures

 Figure 1 shows the pDM12 N-terminal fusion oestrogen receptor DNA binding domain expression vector nucleotide sequence (SEQ ID No 3), between the HindIII and EcoRI restriction sites, comprising a pelB leader secretion sequence (in italics), multiple cloning site containing SfiI and NotI sites, flexible (glycine)₄-serine linker sequence (boxed), a fragment of the oestrogen receptor gene comprising amino acids 176-282 (SEQ ID No 4) of the full length molecule, and the 38 base pair consensus oestrogen receptor DNA binding domain HRE sequence.

Figure 2 shows the OD_{450mm} ELISA data for negative control M13K07 phage, and single-clone PDCP display culture supernatants (#1-4, see Example 3) isolated by selection of the lymphocyte cDNA-pDM12 library against anti-human immunoglobulin kappa antibody.

 Figure 3 shows partial DNA (SEQ ID No 5) and amino acid (SEQ ID No 6) sequence for the human immunoglobulin kappa constant region (Kabat, E. A. et al., Sequences

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of Proteins of Immunological Interest. 4th edition. U.S. Department of Health and Human Services. 1987), and ELISA positive clones #2 (SEQ ID Nos 7 and 8) and #3 (SEQ ID Nos 9 and 10) from Figure 2 which confirms the presence of human kappa constant region DNA in-frame with the pelB leader sequence (pelB leader sequence is underlined, the leader sequence cleavage site is indicated by an arrow). The differences in the 5'-end sequence demonstrates that these two clones were selected independently from the library stock. The PCR primer sequence is indicated in bold, clone #2 was originally amplified with CDNAPCRBAK1 and clone #3 was amplified with CDNAPCRBAK2.

Figure 4 shows the pDM14 N-terminal fusion oestrogen receptor DNA binding domain expression vector nucleotide sequence (SEQ ID No 11), between the HindIII and EcoRI restriction sites, comprising a pelB leader secretion sequence (in italias), multiple cloning site containing SfiI and NotI sites, flexible (glycine)4-serine linker sequence (boxed), a fragment of the oestrogen receptor gene comprising amino acids 176-282 (SEQ ID No 12) of the full length molecule, and the two 38 base pair oestrogen receptor DNA binding domain HRE sequences (HRE 1 and HRE 2).

Figure 5 shows the pDM16 C-terminal fusion oestrogen receptor DNA binding domain expression vector nucleotide sequence (SEQ ID No 13), between the HindIII and EcoRI restriction sites, comprising a pelB leader secretion sequence (in italics), a fragment of the oestrogen receptor gene comprising amino acids 176-282 (SEQ ID No 14) of the full length molecule, flexible (glycine)₄-serine linker sequence (boxed), multiple cloning site containing SfiI and NotI sites and the 38 base pair oestrogen receptor DNA binding domain HRE

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1 sequence.

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Figure 6 shows the OD_{450nm} ELISA data for N-cadherinpDM16 C-terminal display PDCP binding to anti-pancadherin monoclonal antibody in serial dilution ELISA as ampicillin resitance units (a.r.u.). Background binding of negative control M13K07 helper phage is also shown.

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Figure 7 shows the OD_{450mm} ELISA data for *in vivo* biotinylated PCC-pDM16 C-terminal display PDCP binding to streptavidin in serial dilution ELISA as ampicillin resitance units (a.r.u.). Background binding of negative control M13K07 helper phage is also shown.

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Figure 8 shows the OD_{450nm} ELISA data for a human scFv PDCP isolated from a human scFv PDCP display library selected against substance P. The PDCP was tested against streptavidin (1), streptavidin-biotinylated substance P (2), and streptavidin-biotinylated CGRP (3), in the presence (B) or absence (A) of free substance P.

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Figure 9 shows the DNA (SEQ ID Nos 15 and 17) and amino acid (SEQ ID No 16 and 18) sequence of the substance P binding scFv isolated from a human scFv PDCP display library selected against substance P. Heavy chain (SEQ ID Nos 15 and 16) and light chain (SEQ ID Nos 17 and 18) variable region sequence is shown with the CDRs underlined and highlighted in bold.

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Materials and Methods

The following procedures used by the present applicant are described in Sambrook, J., et al., 1989 supra.: restriction enzyme digestion, ligation, preparation of electrocompetent cells, electroporation, analysis of

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restriction enzyme digestion products on agarose gels, DNA purification using phenol/chloroform, preparation of 2xTY medium and plates, preparation of ampicillin, kanamycin, IPTG (Isopropyl β -D-Thiogalactopyranoside) stock solutions, and preparation of phosphate buffered saline.

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Restriction enzymes, T4 DNA ligase and cDNA synthesis reagents (Superscript plasmid cDNA synthesis kit) were purchased from Life Technologies Ltd (Paisley, Scotland, U.K.). Oligonucleotides were obtained from Cruachem Ltd (Glasgow, Scotland, U.K.), or Genosys Biotechnologies Ltd (Cambridge, U.K.). Taq DNA polymerase, Wizard SV plasmid DNA isolation kits, streptavidin coated magnetic beads and mRNA isolation reagents (PolyATract 1000) were obtained from Promega Ltd (Southampton, Hampshire, U.K.). Taqplus DNA polymerase was obtained from Stratagene Ltd (Cambridge, U.K.). PBS, BSA, streptavidin, substance P and anti-pan cadherin antibody were obtained from SIGMA Ltd (Poole, Dorset, U.K.). Anti-M13-HRP conjugated antibody, Kanamycin resistant M13K07 helper bacteriophage and RNAquard were obtained from Pharmacia Ltd (St. Albans, Herts, U.K.) and anti-human Tgk antibody from Harlan-Seralab (Loughborough, Leicestershire, U.K.) Biotinylated substance P and biotinylated calcitonin ...

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Specific embodiments of the invention are given below in Examples 1 to 9.

Peninsula Laboratories (St. Helens, Merseyside, U.K.).

The second of th

gene related peptide (CGRP) were obtained from

31 32 Example 1. Construction of a N-terminal PDCP display phagemid vector pDM12.

The pDM12 vector was constructed by inserting an oestrogen receptor DNA binding domain, modified by appropriate PCR primers, into a phagemid vector pDM6. The pDM6 vector is based on the pUC119 derived phage display vector pHEN1 (Hoogenboom et al., 1991, Nucleic Acids Res. 19: 4133-4137). It contains (Gly) Ser linker, Factor Xa cleavage site, a full length gene III, and streptavidin tag peptide sequence (Schmidt, T.G. and Skerra, A., 1993, Protein Engineering 6: 109-122), all of which can be removed by NotI-EcoRI digestion and agarose gel electrophoresis, leaving a pelB leader sequence, SfiI, NcoI and PstI restriction sites upstream of the digested NotI site. The cloned DNA binding domain is under the control of the lac promoter found in pUC119.

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Preparation of pDM6 with the new problem is a second to the popular of the problem.

The pDM12 vector was constructed by inserting an oestrogen receptor DNA binding domain, modified by appropriate PCR primers, into a phagemid vector pDM6. The pDM6 vector is based on the gene pIII phage display vector pHEN1 (Hoogenboom et al., 1991, Nucleic Acids Res. 19: 4133-4137), itself derived from pUC119 (Viera, J. and Messing, J., 1987, Methods in Enzymol. 153: 3-11). It was constructed by amplifying the pIII gene in pHEN1 with two oligonucleotides:

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PDM6BAK: 5 -TTT TCT GCA GTA ATA GGC GGC CGC AGG GGG AGG

AGG GTC CAT CGA AGG TCG CGA AGC AGA GAC TGT TGA AAG T-3

(SEQ ID No 19) and

36 PDM6FOR: 5 - TTT TGA ATT CTT ATT AAC CAC CGA ACT GCG

GGT GAC GCC AAG CGC TTG CGG CCG TTA AGA CTC CTT ATT ACG CAG-3 (SEQ ID No 20).

and cloning the PstI-EcoRI digested PCR product back into similarly digested pHEN1, thereby removing the c-myc tag sequence and supE TAG codon from pHEN1. The pDM6 vector contains a (Gly) Ser linker, Factor Xa cleavage site, a full length gene III, and streptavidin tag peptide sequence (Schmidt, T.G. and Skerra, A., 1993, Protein Engineering 6: 109-122), all of which can be removed by NotI-EcoRI digestion and agarose gel electrophoresis, leaving a pelB leader sequence, SfiI, NcoI and PstI restriction sites upstream of the digested NotI site. The cloned DNA binding domain is under the control of the lac promoter found in pUC119.

The coestrogen receptor DNA binding domain was isolated from cDNA prepared from human bone marrow (Clontech, Palo Alto, California, U.S.A.). cDNA can be prepared by many procedures well known to those skilled in the art. As an example, the following method using a Superscript plasmid cDNA synthesis kit can be used:

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(a) First strand synthesis.

 $5\mu g$ of bone marrow mRNA, in $5\mu l$ DEPC-treated water was thawed on ice and $2\mu l$ (50pmol) of cDNA synthesis primer (5'-AAAAGCGGCCGCACTGGCCTGAGAGA(N)₆-3') (SEQ ID No 21) was added to the mRNA and the mixture heated to 70°C for 10 minutes, then snap-chilled on ice and spun briefly to collect the contents to the bottom of the tube. The following were then added to the tube:

intermed the second of the gene pitt plage display

 $1\mu l$ 33 1000u/ml RNAguard $1\mu l$ 34 5x first strand buffer $4\mu l$ 35 0.1M DTT $2\mu l$ 36 10mM dNTPs $1\mu l$

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| 1 | 200u/ μ l SuperScript II reverse transcriptase 5 μ l |
|----|--|
| 2 | The mixture was mixed by pipetting gently and incubated |
| 3 | at 37°C for 1 hour, then placed on ice. |
| 4 | |
| 5 | (b) Second strand synthesis. |
| 6 | |
| 7 | The following reagents were added to the first strand |
| 8 | reaction: |
| 9 | DEPC-treated water 93µl |
| 10 | $5x$ second strand buffer $30\mu l$ |
| 11 | 10mM dNTPs 3μ l |
| 12 | 10u/ μ l <i>E. coli</i> DNA ligase 1 μ l |
| 13 | 10u/ μ l E. coli DNA polymerase 4μ l |
| 14 | $2u/\mu l$ E. coli RNase H $1\mu l$ |
| 15 | The reaction was vortex mixed and incubated at 16°C for |
| 16 | 2 hours. $2\mu l$ (10u) of T4 DNA polymerase was added and |
| 17 | incubation continued at 16°C for 5 minutes. The |
| 18 | reaction was placed on ice and 10 μ l 0.5M EDTA added, |
| 19 | then phenol-chloroform extracted, precipitated and |
| 20 | vacuum dried. |
| 21 | |
| 22 | (c) Sal I adaptor ligation. |
| 23 | $\mathcal{L}(\mathcal{G}_{\mathcal{A}}^{(n)}, \mathcal{G}_{\mathcal{A}}^{(n)}) = \mathcal{L}(\mathcal{G}_{\mathcal{A}}^{(n)}, \mathcal{G}_{\mathcal{A}}^{(n)}) = \mathcal{L}(\mathcal{G}_{\mathcal{A}^{(n$ |
| 24 | The cDNA pellet was resuspended in 25 μ l DEPC-treated |
| 25 | water, and ligation set up as follows. |
| 26 | cDNA |
| 27 | $5x$ T4 DNA ligase buffer 10μ l |
| 28 | $1\mu g/\mu l$ Sal I adapters* $10\mu l$ |
| 29 | $1u/\mu lT4$ DNA ligase $5\mu l$ |
| 30 | *Sal I adapters: TCGACCCACGCGTCCG-3' (SEQ ID No 22) |
| 31 | GGGTGCCGAGGC-5' (SEQ ID No 23) |
| 32 | The ligation was mixed gently and incubated for 16 |
| 33 | hours at 16°C, then phenol-chloroform extracted, |

precipitated and vacuum dried. The cDNA/adaptor pellet

was resuspended in $41\mu l$ of DEPC-treated water and

digested with 60 units of NotI at 37°C for 2 hours,

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then phenol-chloroform extracted, precipitated and 1 2 vacuum dried. The cDNA pellet was re-dissolved in 100µl TEN buffer (10mM Tris pH 7.5, 0.1mM EDTA, 25mM NaCl) 3 and size fractionated using a Sephacryl S-500 HR column 4 5 to remove unligated adapters and small cDNA fragments 6 (<400bp) according to the manufacturers instructions. Fractions were checked by agarose gel electrophoresis 7 and fractions containing cDNA less than 400 base pairs 8

discarded, while the remaining fractions were pooled. 9

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(d) PCR amplification of oestrogen receptor DNA binding domain.

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The oestrogen receptor was PCR amplified from $5\mu l$ (150-250ng) of bone marrow cDNA using 25pmol of each of the primers pDM12FOR (SEQ ID No 24) (5'-

17 AAAAGAATTCTGAATGTGTTATTTTAGCTCAGGTCACTCTGACCTGATTATCAAG

ACCCCACTTCACCCCCT) and pDM12BAK (SEQ ID No 25) (5'-18

AAAAGCGGCCGCAGGGGGGGGGGGGTCCATGGAATCTGCCAAGGAG-3') in 19

20 two 50µl reactions containing 0.1mM dNTPs, 2.5 units

Taq DNA polymerase, and 1x PCR reaction buffer (10mM

Tris-HCl pH 9.0, 5mM KCl, 0.01% Triton X -100, 1.5mM 22

MgCl₂) (Promega Ltd, Southampton, U.K.). The pDM12FOR

24 primer anneals to the 3'-end of the DNA binding domain

of the oestrogen receptor and incorporates two stop 25

codons, the 38 base pair consensus oestrogen receptor 26

HRE sequence, and an EcoRI restriction site. The 27

28 pDM12BAK primer anneals to the 5'-end of the DNA

binding domain of the oestrogen receptor and 29

incorporates the (Gly) Ser linker and the NotI

restriction site. 31

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Reactions were overlaid with mineral oil and PCR 33 34 . carried out on a Techne PHC-3 thermal cycler for 30 cycles of 94°C, 1 minute; 65°C, 1 minute; 72°C, 1 35

36 minute. Reaction products were electrophoresed on an

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agarose gel, excised and products purified from the gel using a Geneclean II kit according to the manufacturers instructions (Biol01, La Jolla, California, U.S.A.).

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(e) Restriction digestion and ligation.

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The PCR reaction appended NotI and EcoRI restriction sites, the (Gly) Ser linker, stop codons and the 38 base pair oestrogen receptor target HRE nucleotide sequence to the oestrogen receptor DNA binding domain sequence (see Figure 1). The DNA PCR fragment and the target pDM6 vector (approximately 500ng) were NotI and EcoRI digested for 1 hour at 37°C, and DNA purified by agarose gel electrophoresis and extraction with Geneclean II kit (Bio101, La Jolla, California, U.S.A.). The oestrogen receptor DNA binding domain cassette was ligated into the NotI-EcoRI digested pDM6 vector overnight at 16°C, phenol/chloroform extracted and precipitated then electroporated into TG1 E. coli (genotype: K12, (Δlac-pro), supE, thi, hsD5/F'traD36, proA⁺B⁺, LacI⁴, LacZΔ15) and plated onto 2xTY agar plates supplemented with 1% glucose and 100µg/ml ampicillin. Colonies were allowed to grow overnight at 37°C. Individual colonies were picked into 5ml 2xTY supplemented with 1% glucose and 100 µg/ml ampicillin and grown overnight at 37°C. Double stranded phagemid DNA was isolated with a Wizard SV plasmid DNA isolation kit and the sequence confirmed with a Prism dyedeoxy cycle sequencing kit (Perkin-Elmer, Warrington, Lancashire, U.K.) using M13FOR (SEQ ID No 26) (5'-GTAAAACGACGCCAGT) and M13REV (SEQ ID No 27) (5'-GGATAACAATTTCACACAGG) oligonucleotides. The pDM12 PDCP display vector DNA sequence between the HindIII and EcoRI restriction sites is shown in Figure 1.

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Example 2. Insertion of a random-primed human

lymphocyte cDNA into pDM12 and preparation of a master PDCP stock.

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Libraries of peptides can be constructed by many methods known to those skilled in the art. The example given describes a method for constructing a peptide library from randomly primed cDNA, prepared from mRNA isolated from a partially purified cell population.

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mRNA was isolated from approximately 109 human peripheral blood lymphocytes using a polyATract 1000 mRNA isolation kit (Promega, Southampton, UK). The cell pellet was resuspended in 4ml extraction buffer (4M guanidine thiocyanate, 25mM sodium citrate pH 7.1, 2% β -mercaptoethanol). 8ml of pre-heated (70°C) dilution buffer (6xSSC, 10mM Tris pH 7.4, 1mM EDTA, 0.25% SDS, 1% β -mercaptoethanol) was added to the homogenate and mixed thoroughly by inversion. 10µl of biotinylated oligo-dT (50 pmol/ μ l) was added, mixed and the mixture incubated at 70°C for 5 minutes. The lymphocyte cell lysate was transferred to 6x 2ml sterile tubes and spun at 13,000 rpm in a microcentrifuge for ten minutes at ambient temperature to produce a cleared lysate. During this centrifugation, streptavidin coated magnetic beads were resuspended and 6ml transferred to a sterile 50ml Falcon tube, then placed in the magnetic stand in a horizontal position until all the beads were captured. The supernatant was carefully poured off and beads resuspended in 6ml 0.5xSSC, then the capture repeated. This wash was repeated 3 times, and beads resuspended in a final volume of 6ml 0.5xSSC. The cleared lysate was added to the washed beads, mixed by inversion and incubated at ambient temperature for 2 minutes, then beads captured in the magnetic stand in a horizontal -position. The beads were resuspended gently in 2ml 0.5xSSC and transferred to a sterile 2ml screwtop tube,

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then captured again in the vertical position, and the wash solution discarded. This wash was repeated twice

more. 1ml of DEPC-treated water was added to the beads

4 and mixed gently. The beads were again captured and the

eluted mRNA transferred to a sterile tube. $50\mu l$ was

6 electrophoresed to check the quality and quantity of

7 mRNA, while the remainder was precipitated with 0.1

, midde, while the lemainder was precipitated with oil

8 volumes 3M sodium acetate and three volumes absolute

9 ethanol at -80°C overnight in 4 aliquots in sterile

10 1.5ml screwtop tubes.

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Double stranded cDNA was synthesised as described in

Example 1 using $5\mu g$ of lymphocyte mRNA as template.

14 The cDNA was PCR amplified using oligonucleotides

15 CDNAPCRFOR (SEQ ID No 28) (5'-

16 AAAGCGGCCGCACTGGCCTGAGAGA), which anneals to the cDNA

17 synthesis oligonucleotide described in Example 1 which

18 is present at the 3'-end of all synthesised cDNA

19 molecules incorporates a NotI restriction site, and an

20 equimolar mixture of CDNAPCRBAK1, CDNAPCRBAK2 and

21 CDNAPCRBAK3.

22 CDNAPCRBAK1: (SEQ ID No 29) 5'-

23 AAAAGGCCCAGCCGGCCATGGCCCAGCCCACCACGCGTCCG,

24 CDNAPCRBAK2: (SEQ ID No 30) 5'-

25 AAAAGGCCCAGCCGGCCATGGCCCAGTCCCACGCGTCCG, Tall And the second s

26 CDNAPCRBAK3: (SEQ ID No 31) 5'-

27 AAAAGGCCCAGCCGGCCATGGCCCAGTACCCACCACGCGTCCG),

28 all three of which anneal to the SalI adaptor sequence

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found at the 5'-end of the cDNA and incorporate a SfiI

restriction site at the cDNA 5'-end. Ten PCR reactions

31 were carried out using $2\mu l$ of cDNA (50ng) per reaction

32 as described in Example 1 using 25 cycles of 94°C, 1

minute; 60°C, 1 minute; 72°C, 2 minutes. The reactions

were pooled and a -20μ l aliquot checked by agarose gel

35 electrophoresis, the remainder was phenol/chloroform

36 extracted and ethanol precipitated and resuspended in

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| 1 | $100\mu l$ sterile water. $5\mu g$ of pDM12 vector DNA and |
|----|---|
| 2 | lymphocyte cDNA PCR product were Sfil-NotI digested |
| 3 | phenol/chloroform extracted and small DNA fragments |
| 4 | removed by size selection on Chromaspin 1000 spin |
| 5 | columns (Clontech, Palo Alto, California, U.S.A.) by |
| 6 | centrifugation at 700g for 2 minutes at room |
| 7 | temperature. Digested pDM12 and lymphocyte cDNA were |
| 8 | ethanol precipitated and ligated together for 16 hours |
| 9 | at 16°C. The ligated DNA was precipitated and |
| 10 | electroporated in to TG1 E. coli. Cells were grown in |
| 11 | 1ml SOC medium per cuvette used for 1 hour at 37°C, and |
| 12 | plated onto 2xTY agar plates supplemented with 1% |
| 13 | glucose and $100\mu g/ml$ ampicillin. 10^{-4} , 10^{-5} and 10^{-6} |
| 14 | dilutions of the electroporated bacteria were also |
| 15 | plated to assess library size. Colonies were allowed to |
| 16 | grow overnight at 30°C. 2x108 ampicillin resistant |
| 17 | colonies were recovered on the agar plates. |
| 18 | The bacteria were then scraped off the plates into 40ml |
| 19 | 2xTY broth supplemented with 20% glycerol; 1% glucose |
| 20 | and 100 μ g/ml ampicillin. 5ml was added to a 20ml 2xTY |
| 21 | culture broth supplemented with 1% glucose and $100\mu g/ml$ |
| 22 | ampicillin and infected with 1011 kanamycin resistance |
| 23 | units (kru) M13K07 helper phage at 37°C for 30 minutes |
| 24 | without shaking, then for 30 minutes with shaking at |
| 25 | 200rpm. Infected bacteria were transferred to 200ml |
| 26 | 2xTY broth supplemented with 25µg/ml kanamycin, |
| 27 | $100\mu g/ml$ ampicillin, and $20\mu M$ IPTG, then incubated |
| 28 | overnight at 37°C, shaking at 200rpm. Bacteria were |
| 29 | pelleted at 4000rpm for 20 minutes in 50ml Falcon |
| 30 | tubes, and 40ml 2.5M NaCl/20% PEG 6000 was added to |
| 31 | 200ml of particle supernatant, mixed vigorously and |
| 32 | incubated on ice for 1 hour to precipitate PDCP |
| 33 | particles. Particles were pelleted at 11000rpm for 30 |
| 34 | minutes in 250ml Oakridge tubes at 4°C in a Sorvall |
| 35 | RC5B centrifuge, then resuspended in 2ml PBS buffer |
| 36 | after removing all traces of PEG/NaCl with a pipette, |

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then bacterial debris removed by a 5 minute 13500rpm spin in a microcentrifuge. The supernatent was filtered through a $0.45\mu m$ polysulfone syringe filter and stored at -20°C.

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Example 3. Isolation of human immunoglobulin kappa light chains by repeated rounds of selection against anti-human kappa antibody.

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For the first round of library selection a 70x11mm NUNC Maxisorp Immunotube (Life Technologies, Paisley, Scotland U.K.) was coated with 2.5ml of $10\mu g/ml$ of anti-human kappa antibody (Seralab, Crawley Down, Sussex, U.K.) in PBS for 2 hours at 37°C. The tube was rinsed three times with PBS (fill & empty) and blocked with 3ml PBS/2% BSA for 2 hours at 37°C and washed as: before. 4x10¹² a.r.u. of pDM12-lymphocyte cDNA PDCP stock was added in 2ml 2% BSA/PBS/0.05% Tween 20, and incubated for 30 minutes on a blood mixer, then for 90 minutes standing at ambient temperature. The tube was washed ten times with PBS/0.1% Tween 20, then a further ten times with PBS only. Bound particles were eluted in 1ml of freshly prepared 0.1M triethylamine for 10 minutes at ambient temperature on a blood mixer. Eluted particles were transferred to 0.5ml 1M Tris pH 7.4, vortex mixed briefly and transferred to ice.

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Neutralised particles were added to 10ml log phase TG1 E coli bacteria (optical density: OD_{600nm} 0.3-0.5) and incubated at 37°C without shaking for 30 minutes, then with shaking at 200rpm for 30 minutes. 10^{-3} , 10^{-4} & 10^{-5} dilutions of the infected culture were prepared to estimate the number of particles recovered, and the remainder was spun at 4000 rpm for 10 minutes, and the pellet resuspended in $300\mu l$ 2xTY medium by vortex mixing. Bacteria were plated onto 2xTY agar plates

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supplemented with 1% glucose and $100\mu g/ml$ ampicillin. Colonies were allowed to grow overnight at 30°C.

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A PDCP stock was prepared from the bacteria recovered from the first round of selection, as described in Example 2 from a 100ml overnight culture. 250µl of the round 1 amplified PDCP stock was then selected against anti-human kappa antibody as described above with the tube was washed twelve times with PBS/0.1% Tween 20, then a further twelve times with PBS only.

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To identify selected clones, eighty-eight individual clones recovered from the second round of selection were then tested by ELISA for binding to anti-human kappa antibody. Individual colonies were picked into 100μ l 2xTY supplemented with 100μ g/ml ampicillin and 1% glucose in 96-well plates (Costar) and incubated at 37°C and shaken at 200rpm for 4 hours. 25µl of each culture was transferred to a fresh 96-well plate, containing 25μ l/well of the same medium plus 10^7 k.r.u. M13K07 kanamycin resistant helper phage and incubated hat 37°C for 30 minutes without shaking, then incubated at 37°C and shaken at 200rpm for a further 30 minutes. 160µl of 2xTY supplemented with 100µg/ml ampicillin, 25μg/ml kanamycin, and 20μM IPTG was added to each well and particle amplification continued for 16 hours at 37°C while shaking at 200rpm. Bacterial cultures were spun in microtitre plate/carriers at 2000g for 10 minutes at 4°C in a benchtop centrifuge to pellet bacteria and culture supernatant used for ELISA.

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A Dynatech Immulon 4 ELISA plate was coated with 200ng/well anti-human kappa antibody in 100μ l /well PBS for one hour at $37\,^{\circ}$ C. The plate was washed $2x200\mu$ l/well PBS and blocked for 1 hour at $37\,^{\circ}$ C with 200μ l/well 2% BSA/PBS and then washed $2x200\mu$ l/well PBS. 50μ l PDCP

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culture supernatant was added to each well containing 50μl/well 4% BSA/PBS/0.1%Tween 20, and allowed to bind for 1 hour at ambient temperature. The plate was washed three times with $200\mu l/well$ PBS/0.1% Tween 20, then three times with 200μ l/well PBS. Bound PDCPs were detected with 100 μ l/well, 1:5000 diluted anti-M13-HRP conjugate (Pharmacia) in 2% BSA/PBS/0.05% Tween 20 for 1 hour at ambient temperature and the plate washed six times as above. The plate was developed for 5 minutes at ambient temperature with 100µl/well freshly prepared TMB (3,3',5,5'-Tetramethylbenzidine) substrate buffer (0.005% H₂O₂, 0.1mg/ml TMB in 24mM citric acid/52mM sodium phosphate buffer pH 5.2). The reaction was stopped with 100 μ l/well 12.5% $m H_2SO_4$ and read at 450nm. (ELISA data for binding clones is shown in Figure 2). The Balling of the Control of the Co

These clones were then sequenced with M13REV primer (SEQ ID No 27) as in Example 1. The sequence of two of the clones isolated is shown in Figure 3 (see SEQ ID Nos 7 tox10). Figure 3 (see SEQ ID

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Example 479 Construction of the pDM14 N-terminal display vectors a 2 th multiplication of the Laborator with the statement of the statement of

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It would be useful to design vectors that contain a second DBD binding sequence, such as a second oestrogen receptor HRE sequence, thus allowing the display of increased numbers of peptides per PDCP. Peale et al. (1988, Proc. Natl. Acad. Sci. USA 85: 1038-1042) describe a number of oestrogen receptor HRE sequences. These sequences were used to define an HRE sequence, which differs from that cloned in pDM12, which we used to create a second N-terminal display vector (pDM14). The oligonucleotide: 5'-AAAAGAATTCGAGGTTACATTAACTTTGTT CCGGTCAGACTGACCCAAGTCGACCTGAATGTGTTATTTTAG-3' (SEQ ID No 32) was synthesised and used to mutagenise pDM12 by

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1 PCR with pDM12BAK oligonucleotide as described in 2 Example 1 using 100ng pDM12 vector DNA as template. The resulting DNA fragment, which contained the oestrogen 3 4 receptor DBD and two HRE sequences separated by a SalI 5 restriction enzyme site, was NotI-EcoRI restriction enzyme digested and cloned into NotI-EcoRI digested 6 7 pDM12 vector DNA as described in Example 1 to create pDM14. The sequence of pDM14 between the HindIII and 8 . .9 EcoRI restriction enzyme sites was checked by DNA 10 sequencing. The final vector sequence between these two sites is shown in Figure 4 (see SEQ ID Nos 11 and 12). 11

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Example 5. Construction of the pDM16 C-terminal display vector

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In order to demonstrate the display of peptides fused to the C-terminus of a DBD on a PDCP a suitable vector, pDM16, was created.

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In pDM16 the pelB leader DNA sequence is fused directly to the oestrogen receptor DBD sequence removing the multiple cloning sites and the Gly4Ser linker DNA sequence found in pDM12 and pDM14, which are appended to the C-terminal end of the DBD sequence upstream of the HRE DNA sequence to the contract of the ball the sequence of the ball the se

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To create this vector two separate PCR reactions were carried out on a Techne Progene thermal cycler for 30 cycles of 94°C, 1 minute; 60°C, 1 minute; 72°C, 1 minute. Reaction products were electrophoresed on an agarose gel, excised and products purified from the gel using a Mermaid or Geneclean II kit, respectively, according to the manufacturers instructions (Bio101, La Jolla, California, U.S.A.).

മാം ഇന്ത്യായുടെ നേരും വരുന്നു. അവരു വരുന്നു വരുന്നു വരുന്നു വരുന്നു. വരുന്നു വരുന്നു വരുന്നു വരുന്നു വരുന്നു വരുന്നു വരുന്നു വരുന്നു.

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In the first, the 5'-untranslated region and pelB

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leader DNA sequence was amplified from 100ng of pDM12
vector DNA using 50pmol of each of the oligonucleotides
pelBFOR (SEQ ID No 33) (5'-CCTTGGCAGATTCCATCT
CGGCCATTGCCGGC-3') and M13REV (SEQ ID NO 27) (see
above) in a 100µl reaction containing 0.1mM dNTPs, 2.5
units Taqplus DNA polymerase, and 1x High Salt PCR
reaction buffer (20mM Tris-HCl pH 9.2, 60mM KCl, 2mM

8 MgCl₂) (Stratagene Ltd, Cambridge, U.K.).

1.00 9 In the second, the 3'-end of the pelB leader sequence 10 and the oestrogen receptor DBD was amplified from 100ng 11 of pDM12 vector DNA using 50pmol of each of the 12 oligonucleotides pelBBAK (SEQ ID No 34) (5'-CCGGCAA 13 TGGCCGAGATGGAATCTGCCAAGG-3') and pDM16FOR (SEQ ID No 14 35) (5'-TTTTGTCGACTCAATCAGTTATGCGGCCGCCAGCTGCAGG 15 AGGGCCGGCTGGGCCGACCCTCCCCCCAGACCCCACTTCACCCC-3') in a 16 100µl reaction containing 0.1mM dNTPs, 2.5 units 17

Taqplus DNA polymerase, and 1x High Salt PCR reaction buffer (Stratagene Ltd, Cambridge, U.K.). Following gel purification both products were mixed together and a final round of PCR amplification carried out to link the two products together as described above, in a 100μl reaction containing 0.1mM dNTPs, 2.5 units Taq DNA polymerase, and 1x PCR reaction buffer (10mM Tris-

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25 , HCl pH 9, 0, 5mM KCl, 0.01% Triton X -100, 1.5mM MgCl₂)

26 (Promega Ltd, Southampton, U.K.).

2728 The resulting DM

The resulting DNA fragment, was HindIII-SalI restriction enzyme digested and cloned into HindIII-SalI digested pDM14 vector DNA as described in Example 1 to create pDM16. The sequence of pDM16 between the HindIII and EcoRI restriction enzyme sites was checked by DNA sequencing. The final vector sequence between these two sites is shown in Figure 5 (see SEQ ID Nos 13)

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Example 6. Display of the C-terminal fragment of human
N-cadherin on the surface of a PDCP

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cDNA libraries of peptides can be constructed by many methods known to those skilled in the art. One commonly used method for constructing a peptide library uses oligo dT primed cDNA, prepared from polyA+ mRNA. In this method the first-strand synthesis is carried out using an oligonucleotide which anneals to the 3'-end polyA tail of the mRNA composed of T, (where n is normally between 10 and 20 bases) and a restriction enzyme site such as NotI to facilitate cloning of cDNA. The cDNA cloned by this method is normally composed of the polyA tail, the 3'- end untranslated region and the C-terminal coding region of the protein. As an example of the C-terminal display of peptides on a PDCP, a human cDNA isolated from a library constructed by the above method was chosen. 1. 1. 1

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The protein N-cadherin is a cell surface molecule involved in cell-cell adhesion. The C-terminal cytoplasmic domain of the human protein (Genbank database accession number: M34064) is recognised by a commercially available monoclonal antibody which was raised against the C-terminal 23 amino acids of chicken N-cadherin (SIGMA catalogue number: C-1821). The 1.4kb human cDNA fragment encoding the C-terminal 99 amino acids, 3'- untranslated region and polyA tail (NotI site present at the 3'-end of the polyA tail) was amplified from approximately 20ng pDM7-NCAD#C with 25pmol of each oligonucleotide M13FOR (SEQ ID No 26) and CDNPCRBAK1 (SEQ ID No 29) (see above) in a 50μ l reaction containing 0.1mM dNTPs, 2.5 units Tagplus DNA polymerase, and 1x High Salt PCR reaction buffer (20mM Tris-HCl pH 9.2, 60mM KCl, 2mM MgCl₂) (Stratagene Ltd, Cambridge, U.K.) on a Techne Progene thermal cycler for

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30 cycles of 94°C, 1 minute; 60°C, 1 minute; 72°C, 1 minute. Following gel purification and digestion with SfiI and NotI restiction enzymes, the PCR product was cloned into pDM16 using an analogous protocol as described in Example 1.

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Clones containing inserts were identified by ELISA of 96 individual PDCP cultures prepared as described in Example 3. A Dynatech Immulon 4 ELISA plate was coated with 1:250 diluted anti-pan cadherin monoclonal antibody in 100µl /well PBS overnight at 4°C. The plate was washed $3x200\mu l/well$ PBS and blocked for 1 hour at 37°C with 200µl/well 2% Marvel non-fat milk powder/PBS and then washed 2x200µl/well PBS. 50µl PDCP culture supernatant was added to each well containing $50\mu l/well$ 4% Marvel/PBS, and allowed to bind for 1 hour at ambient temperature. The plate was washed three times with $200\mu l/well$ PBS/0.1% Tween 20, then three times with 200µ1/well PBS. Bound PDCPs were detected with 100µl/well, 1:5000 diluted anti-M13-HRP conjugate (Pharmacia) in 2% Marvel/PBS for 1 hour at ambient temperature and the plate washed six times as above. The plate was developed for 15 minutes at ambient temperature with 100μ l/well freshly prepared TMB (3,3',5,5'-Tetramethylbenzidine) substrate buffer (0.005% H₂O₂, 0.1mg/ml TMB in 24mM citric acid/52mM sodium phosphate buffer pH 5.2). The reaction was stopped with 100μ l/well 12.5% H_2SO_4 and read at 450nm. The nucleotide sequence of an ELISA positive clone insert and DBD junction was checked by DNA sequencing using oligonucleotides M13FOR (SEQ ID No 26) (see Example 1) and ORSEQBAK (SEQ ID No 36) (5'-TGTTGAAACACAAGCGCCAG-3').

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A fifty-fold concentrated stock of C-terminal Ncadherin PDCP particles was prepared by growing the un-

infected TG1 clone in 1ml 2xTY culture broth supplemented with 1% glucose and 100µg/ml ampicillin for five hours at 37°C, shaking at 200rpm and infecting with 108 kanamycin resistance units (kru) M13K07 helper phage at 37°C for 30 minutes without shaking, then for 30 minutes with shaking at 200rpm. Infected bacteria were transferred to 20ml 2xTY broth supplemented with $25\mu g/ml$ kanamycin, $100\mu g/ml$ ampicillin, and $20\mu M$ IPTG, then incubated overnight at 30°C, shaking at 200rpm. Bacteria were pelleted at 4000rpm for 20 minutes in 50ml Falcon tubes, and 4ml 2.5M NaCl/20% PEG 6000 was added to 20ml of PDCP supernatant, mixed vigorously and incubated on ice for 1 hour to precipitate particles.

The particles were pelleted at 11000rpm for 30 minutes in 50ml Oakridge tubes at 4°C in a Sorvall RC5B centrifuge, then resuspended in PBS buffer after removing all traces of PEG/NaCl with a pipette, then bacterial debris removed by a 5 minute 13500rpm spin in a microcentrifuge. The supernatant was filtered through a $0.45\mu m$ polysulfone syringe filter. The concentrated stock was two-fold serially diluted and used in ELISA against plates coated with anti-pan-cadherin antibody as described above (see Figure 6).

 This example demonstrates the principle of C-terminal display using PDCPs, that C-terminal DBD-peptide fusion PDCPs can be made which can be detected in ELISA, and the possibility that oligo dT primed cDNA libraries may be displayed using this method.

Example 7. Display of *in vivo* biotinylated C-terminal domain of human propionyl CoA carboxylase on the surface of a PDCP

Example 6 shows that the C-terminal domain of human N-

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cadherin can be expressed on the surface of a PDCP as a C-terminal fusion with the DBD. Here it is shown that the C-terminal domain of another human protein propionyl CoA carboxylase alpha chain (Genbank accession number: X14608) can similarly be displayed, suggesting that this methodology may be general.

The alpha sub-unit of propionyl CoA carboxylase alpha chain (PCC) contains 703 amino acids and is normally biotinylated at position 669. It is demonstrated that the PCC peptide displayed on the PDCP is biotinylated, as has been shown to occur when the protein is expressed in bacterial cells (Leon-Del-Rio & Gravel; 1994, J. Biol. Chem. 37, 22964-22968).

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The 0.8kb human cDNA fragment of PCC alpha encoding the C-terminal 95 amino acids, 3'- untranslated region and polyA tail (NotI site present at the 3'-end of the polyA tail) was amplified and cloned into pDM16 from approximately 20ng pDM7-PCC#C with 25pmol of each oligonucleotide M13FOR (SEQ ID No 26) and CDNPCRBAK1 (SEQ ID No 29) as described in Example 6.

Clones containing inserts were identified by ELISA as described in Example 6, except that streptavidin was coated onto the ELISA plate at 250ng/well, in place of the anti-cadherin antibody. The nucleotide sequence of an ELISA positive clone insert and DBD junction was checked by DNA sequencing using oligonucleotides M13FOR (SEQ ID No 26) and ORSEQBAK (SEQ ID No 36) (see above). A fifty-fold concentrated stock of C-terminal PCC PDCP particles was prepared and tested in ELISA against streptavidin as described in Example 6 (see Figure 7).

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This example shows not only that the peptide can be displayed as a C-terminal fusion on a PDCP, but also

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that in vivo modified peptides can be displayed.

used are detailed in Table 1.

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Example 8. Construction of a human scFv PDCP display
library

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This example describes the generation of a human antibody library of scFvs made from an un-immunised human. The overall strategy for the PCR assembly of scFv fragments is similar to that employed by Marks, J. D. et al. 1991, J. Mol. Biol. 222: 581-597. The antibody gene oligonucleotides used to construct the library are derived from the Marke et al., paper and from sequence data extracted from the Kabat database (Kabat, E. A. et al., Sequences of Proteins of Immunological Interest. 4th edition. U.S. Department of Health and Human Services. 1987). The three linker oligonucleotides are described by Zhou et al. (1994, Nucleic Acids Res., 22: 888-889), all oligonucleotides

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First, mRNA was isolated from peripheral blood lymphocytes and cDNA prepared for four repertoires of antibody genes IgD, IgM, Ig κ and Ig λ , using four separate cDNA synthesis primers. VH genes were amplified from IgD and IgM primed cDNA, and VL genes were amplified from $Ig\kappa$ and $Ig\lambda$ primed cDNA. A portion of each set of amplified heavy chain or light chain DNA was then spliced with a separate piece of linker DNA encoding the 15 amino acids (Gly Ser), (Huston, J. S. et al. 1989, Gene, 77: 61). The 3'-end of the VH PCR products and the 5'-end of the VL PCR products overlap the linker sequence as a result of incorporating linker sequence in the JH, $V\kappa$ and $V\lambda$ family primer sets (Table 1). Each VH-linker or linker-VL DNA product was then spliced with either VH or VL DNA to produce the primary scFv product in a VH-linker-VL configuration. This scFv

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product was then amplified and cloned into pDM12 as a SfiI-NotI fragment, electroporated into TG1 and a

3 concentrated PDCP stock prepared.

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mRNA isolation and cDNA synthesis.

6 Human lymphocyte mRNA was purified as described in

Example 2. Separate cDNA reactions were performed with

8 IGDCDNAFOR (SEQ ID No 37), IGMCDNAFOR (SEQ ID No 38),

9 IGKCDNAFOR (SEQ ID No 39) and IGλCDNAFOR (SEQ ID No 40)

10 oligonucleotides. 50pmol of each primer was added to

11 approximately $5\mu g$ of mRNA in $20\mu l$ of nuclease free

water and heated to 70°C for 5 minutes and cooled

13 rapidly on ice, then made up to a final reaction volume

of 100μ l containing 50mM Tris pH 8.3, 75mM KCl, 3mM

15 MgCl₂, 10mM DTT, 0.5mM dNTPs, and 2000 units of

Superscript II reverse transcriptase (Life

17 Technologies, Paisley, Scotland, U.K.). The reactions

were incubated at 37°C for two hours, then heated to

95°C for 5 minutes.

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Primary PCRs.

For the primary PCR amplifications separate amplifications were set up for each family specific primer with either an equimolar mixture of the JHFOR primer set (SEQ ID Nos 41 to 44) for IgM and IgD cDNA, or with SCFVκFOR (SEQ ID No 51) or SCFVλFOR (SEQ ID No 52) for IgK or Igλ cDNA respectively e.g. VH1BAK and JHFOR set; Vκ2BAK (SEQ ID No 54) and SCFVκFOR (SEQ ID No 51); Vλ3aBAK (SEQ ID No 66) and SCFVλFOR (SEQ ID No 52) etc. Thus, for IgM, IgD and Igκ cDNA six separate reactions were set up, and seven for Igλ cDNA. A 50μl reaction mixture was prepared containing 2μl cDNA, 25pmol of the appropriate FOR and BAK primers, 0.1mM dNTPs, 2.5 units Taqplus-DNA polymerase, and 1x High Salt PCR reaction buffer (20mM Tris-HCl pH 9.2, 60mM

KCl, 2mM MgCl₂) \((Stratagene Ltd, Cambridge, U.K.).

Reactions were amplified on a Techne Progene thermal cycler for 30 cycles of 94°C, 1 minute; 60°C, 1 minute; 72°C, 2 minutes, followed by 10 minutes at 72°C. Fifty microlitres of all 25 reaction products were electrophoresed on an agarose gel, excised and products purified from the gel using a Geneclean II kit according to the manufacturers instructions (Bio101, La

Jolla, California, U.S.A.). All sets of IgD, IgM, IgK or Igλ reaction products were pooled to produce VH or

or 1gh reaction products were pooled to produce vh or

VL DNA sets for each of the four repertoires. These

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VL DNA sets for each of the four repertoires. These

were then adjusted to approximately $20 \text{ng}/\mu 1$.

Preparation of linker.

Linker product was prepared from eight 100µl reactions containing 5ng LINKAMP3T (SEQ ID No 76) template oligonucleotide, 50pmol of LINKAMP3 (SEQ ID No 74) and LINKAMP5 (SEQ ID No 75) primers, 0.1mM dNTPs, 2.5 units Taqplus DNA polymerase, and 1x High Salt PCR reaction buffer (20mM Tris-HCl pH 9.2, 60mM KCl, 2mM MgCl₂) (Stratagene Ltd, Cambridge, U.K.). Reactions were amplified on a Techne Progene thermal cycler for 30 cycles of 94°C, 1 minute; 60°C, 1 minute; 72°C, 1 minute, followed by 10 minutes at 72°C. All reaction product was electrophoresed on a 2% low melting point agarose gel, excised and products purified from the gel using a Mermaid kit according to the manufacturers instructions (Biol01, La Jolla, California, U.S.A.) and adjusted to 5ng/µl.

First stage linking.

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Four linking reactions were prepared for each repertoire using 20ng of VH or VL DNA with 5ng of Linker DNA in 100μl reactions containing (for IgM or IgD VH) 50pmol of LINKAMPFOR and VH1-6BAK set, or, 50pmol LINKAMPBAK and either SCFVκFOR (Igκ) or SCFVλFOR (Igλ), 0.1mM dNTPs, 2.5 units Tag DNA polymerase, and

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1x PCR reaction buffer (10mM Tris-HCl pH 9.0, 5mM KCl, 1 0.01% Triton X"-100, 1.5mM MgCl₂) (Promega Ltd, 2 Southampton, U.K.). Reactions were amplified on a 3 Techne Progene thermal cycler for 30 cycles of 94°C, 1 4 minute; 60°C, 1 minute; 72°C, 2 minutes, followed by 10 5 minutes at 72°C. Reaction products were electrophoresed 6 on an agarose gel, excised and products purified from 7 the gel using a Geneclean II kit according to the 8 manufacturers instructions (Bio101, La Jolla, 9

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10 California, U.S.A.) and adjusted to $20 \text{ng}/\mu 1$.

Final linking and reamplification.

To prepare the final scFv DNA products, five 100μ l reactions were performed for VH-LINKER plus VL DNA, and, five 100µl reactions were performed for VH plus LINKER-VL DNA for each of the four final repertoires (IgM VH-VK, VH-Vλ; IgD VH-VK, VH-Vλ) as described in (step (d) above using 20ng of each component DNA as template. Reaction products were electrophoresed on an agarose gel, excised and products purified from the gel using a Geneclean II kit according to the manufacturers instructions (Bio101, La Jolla, California, U.S.A.) and adjusted to $20 \text{ng}/\mu 1$. Each of the four repertoires was then re-amplified in a 100µl reaction volume containing 2ng of each linked product, with 50pmol VHBAK1-6 (SEQ ID Nos 53 to 58) and either the JKFOR (SEQ ID Nos 66 to 70) or JAFOR (SEQ ID Nos 71 to 73) primer sets, in the presence of 0.1mM dNTPs, 2.5 units Taq DNA polymerase, and 1x PCR reaction buffer (10mM Tris-HCl pH 9.0, 5mM KC1, 0.01% Triton X -100, 1.5mM MgCl₂) (Promega Ltd, ... Southampton, U.K.). Thirty reactions were performed per repertoire to generate enough DNA for cloning. Reactions were amplified on a Techne Progene thermal -cycler for 25 cycles of 94°C, 1 minute; 65°C, 1 minute; 72°C, 2 minutes, followed by 10 minutes at 72°C. Reaction products were phenol-chloroform extracted,

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ethanol precipitated, vacuum dried and re-suspended in 1 80µl nuclease free water. 2

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Cloning into pDM12.

4 Each of the four repertoires was Sfil-Notl digested, 5 6 and electrophoresed on an agarose gel, excised and 7 products purified from the gel using a Geneclean II kit according to the manufacturers instructions (Bio101, La 8 9 Jolla, California, U.S.A.). Each of the four repertoires was ligated overnight at 16°C in 140µl with 10 10μg of SfiI-NotI cut pDM12 prepared as in Example 2, 11 and 12 units of T4 DNA ligase (Life Technologies, 12 Paisley, Scotland, U.K.). After incubation the 13 ligations were adjusted to $200\mu l$ with nuclease free 14 15 water, and DNA precipitated with 1µl 20mg/ml glycogen, 16 100μ l 7.5M ammonium acetate and 900μ l ice-cold (-20°C) absolute ethanol, vortex mixed and spun at 13,000rpm 17 18 for 20 minutes in a microfuge to pellet DNA. The pellets were washed with 500µl ice-cold 70% ethanol by 19 20 centrifugation at 13,000rpm for 2 minutes, then vacuum dried and re-suspended in $10\mu l$ DEPC-treated water. $1\mu l$ 21 aliquots of each repertoire was electroporated into 22 80µ1 E. coli (TG1). Cells were grown in 1ml SOC medium 23 per cuvette used for 1 hour at 37°C, and plated onto 24 25 2xTY agar plates supplemented with 1% glucose and . $_{2}$ 100 μ g/ml ampicilling 10⁻⁴, 10⁻⁵ and 10⁻⁶ dilutions of the 26 27 electroporated bacteria were also plated to assess library size. Colonies were allowed to grow overnight 28

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Preparation of PDCP stock.

repertoire of 1.21x109 clones.

34 Separate PDCP stocks were prepared for each repertoire

library. The bacteria were then scraped off the plates 35

into 30ml 2xTY broth supplemented with 20% glycerol, 1%

at 30°C. Cloning into Sfil-NotI digested pDM12 yielded

an IgM- κ/λ repertoire of 1.16x10° clones, and an IgD- κ/λ

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| 1 | glucose and 100 μ g/ml ampicillin. 3ml was added to a |
|----|---|
| 2 | 50ml 2xTY culture broth supplemented with 1% glucose |
| 3 | and $100\mu g/ml$ ampicillin and infected with 10^{11} kanamycin |
| 4 | resistance units (kru) M13K07 helper phage at 37°C for |
| 5 | 30 minutes without shaking, then for 30 minutes with |
| 6 | shaking at 200rpm. Infected bacteria were transferred |
| 7 | to 500ml 2xTY broth supplemented with $25\mu g/ml$ |
| 8 | kanamycin, 100 μ g/ml ampicillin, and 20 μ M IPTG, then |
| 9 | incubated overnight at 30°C, shaking at 200rpm. |
| 10 | Bacteria were pelleted at 4000rpm for 20 minutes in |
| 11 | 50ml Falcon tubes, and 80ml 2.5M NaCl/20% PEG 6000 was |
| 12 | added to 400ml of particle supernatant, mixed |
| 13 | vigorously and incubated on ice for 1 hour to |
| 14 | precipitate PDCP particles. Particles were pelleted at |
| 15 | 11000rpm for 30 minutes in 250ml Oakridge tubes at 4°C |
| 16 | in a Sorvall RC5B centrifuge, then resuspended in 40ml |
| 17 | water and 8ml 2.5M NaCl/20% PEG 6000 added to |
| 18 | reprecipitate particles, then incubated on ice for 20 |
| 19 | minutes. Particles were again pelleted at 11000rpm for |
| 20 | 30 minutes in 50ml Oakridge tubes at 4°C in a Sorvall |
| 21 | RC5B centrifuge, then resuspended in 5ml PBS buffer, |
| 22 | after removing all traces of PEG/NaCl with a pipette. |
| 23 | Bacterial debris was removed by a 5 minute 13500rpm |
| 24 | spin in a microcentrifuge. The supernatant was filtered |
| 25 | through a 0.45 μ m polysulfone syringe filter, adjusted |
| 26 | to 20% glycerol and stored at -70°C. |
| 27 | and the second of the control of the |

Example 9. Isolation of binding activity from a N-100 terminal display PDCP library of human scFvs (1)

The ability to select binding activities to a target of interest from a human antibody library is important due to the possibility of generating therapeutic human antibodies. In addition, such libraries allow the isolation of antibodies to targets which cannot be used for traditional methods of antibody generation due to

1 toxicity, low immunogenicity or ethical considerations.

- 2 In this example we demonstrate the isolation of
- 3 specific binding activities against a peptide antigen
- 4 from a PDCP library of scFvs from an un-immunised

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5 human.

 The generation of the library, used for the isolation of binding activities in this example, is described in Example 8.

Substance P is an eleven amino acid neuropeptide involved in inflammatory and pain responses in vivo. It has also been implicated in a variety of disorders such as psoriasis and asthma amongst others (Misery, L. 1997, Br. J. Dertmatol., 137: 843-850; Maggi, C. A. 1997, Regul. Pept. 70: 75-90; Choi, D. C. & Kwon, O.J., 1998, Curr. Opin. Pulm. Med., 4: 16-24). Human antibodies which neutralise this peptide may therefore have some therapeutic potential. As this peptide is too small to coat efficiently on a tube, as described in Example 3, selection of binding activities was performed in-solution, using N-terminal biotinylated substance P and capturing bound PDCP particles on

Enrichment for substance P binding PDCP particles. An aliquot of approximately 10^{13} a.r.u. IgM and IgD scFv library stock was mixed with $1\mu g$ biotinylated substance P in $800\mu l$ 4% BSA/0.1% Tween 20/PBS, and allowed to bind for two hours at ambient temperature. Bound PDCPs were then captured onto 1ml of BSA blocked streptavidin coated magnetic beads for 10 minutes at ambient temperature. The beads were captured to the side of the tube with a magnet (Promega), and unbound material discarded. The beads were washed eight times with 1ml

streptavidin-coated magnetic beads. Agree 1980 1980 1980

PBS/0.1% Tween 20/ 10µg/ml streptavidin, then two times

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with 1ml of PBS by magnetic capture and removal of wash buffer. After the final wash bound PDCPs were eluted with 1ml of freshly prepared 0.1M triethylamine for 10 minutes, the beads were captured, and eluted particles transferred to 0.5ml 1M Tris-HCl pH 7.4. Neutralised particles were added to 10ml log phase TG1 E. coli bacteria and incubated at 37°C without shaking for 30 minutes, then with shaking at 200rpm for 30 minutes. 10⁻³, 10⁻⁴ & 10⁻⁵ dilutions of the infected culture were prepared to estimate the number of particles recovered, and the remainder was spun at 4000 rpm for 10 minutes, and the pellet resuspended in 300μ l 2xTY medium by vortex mixing. Bacteria were plated onto 2xTY agar plates supplemented with 1% glucose and $100\mu g/ml$ ampicillin. Colonies were allowed to grow overnight at 30°C. A 100-fold concentrated PDCP stock was prepared from a 200ml amplified culture of these bacteria as described above, and 0.5ml used in as second round of selection with 500ng biotinylated substance P. For this round 100µg/ml streptavidin was included in the wash buffer.

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ELISA identification of binding clones.

24 Binding clones were identified by ELISA of 96

25 individual PDCP cultures prepared as described in

Example 3 from colonies recovered after the second

27 round of selection. A Dynatech Immulon 4 ELISA plate

28 was coated with 200ng/well streptavidin in 100μ l /well

29 PBS for 1 hour at 37°C. The plate was washed

30 3x200μl/well PBS and incubated with 10ng/well

31 biotinylated substance P in 100μ l /well PBS for 30

32 minutes at 37°C The plate was washed $3x200\mu$ 1/well PBS

33 and blocked for 1 hour at 37°C with 200μ l/well 2%

34 Marvel non-fat milk powder/PBS and then washed

 $2x200\mu$ l/well PBS. 50μ l PDCP culture supernatant was

added to each well containing 50µl/well 4% Marvel/PBS,

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1 and allowed to bind for 1 hour at ambient temperature. The plate was washed three times with $200\mu l/well$ 2 3 PBS/0.1% Tween 20, then three times with 200μ l/well PBS. Bound PDCPs were detected with 100μ l/well, 1:5000 4 5 diluted anti-M13-HRP conjugate (Pharmacia) in 2% Marvel/PBS for 1 hour at ambient temperature and the 6 7 plate washed six times as above. The plate was developed for 10 minutes at ambient temperature with 8 9 100μ l/well freshly prepared TMB (3,3',5,5'-Tetramethylbenzidine) substrate buffer (0:005% H₂O₂, 10 11 0.1mg/ml TMB in 24mM citric acid/52mM sodium phosphate 12 buffer pH 5.2). The reaction was stopped with 13 $100\mu l/well$ 12.5% H_2SO_4 and read at 450nm. Out of 96 14 clones tested, 10 gave signals greater than twice background (background = 0.05). 15

Characterization of a binding clone.

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A 50-fold concentrated PDCP stock was prepared from a 100ml amplified culture of a single ELISA positive clone as described above. 10µl per well of this stock was tested in ELISA as described above for binding to streptavidin, streptavidin-biotinylated-substance P and streptavidin-biotinylated-CGRP (N-terminal: biotinylated). Binding was only observed in the control of the con streptavidin-biotinylated-substance P coated wells indicating that binding was specific. In addition, binding to streptavidin-biotinylated substance P was completely inhibited by incubating the PDCP with $1\mu g/ml$ free substance P (see Figure 8). The scFv VH (SEQ ID Nos 15 and 16) and VL (SEQ ID Nos 17 and 18) DNA and amino acid sequence was determined by DNA sequencing with oligonucleotides M13REV (SEQ ID No27) and ORSEQFOR (SEQ ID No 36) and is shown in Figure 9.

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The results indicate that target binding activities can be isolated from PDCP display libraries of human scFv

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1 fragments.

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Example 10

In another example the invention provides methods for screening a DNA library whose members require more than 5 one chain for activity, as required by, for example, 6 antibody Fab fragments for ligand binding. To increase 7 the affinity of an antibody of known heavy and light 8 chain sequence, libraries of unknown light chains 9 co-expressed with a known heavy chain are screened for 10 higher affinity antibodies. The known heavy chain 11 antibody DNA sequence is joined to a nucleotide 12 sequence encoding a oestrogen receptor DNA binding 13 domain in a phage vector which does not contain the 14 oestrogen receptor HRE sequence. The antibody DNA 15 sequence for the known heavy chain (VH and CH1) gene is 16 inserted in the 5' region of the oestrogen receptor DBD 17 18 DNA, behind an appropriate promoter and translation 19 sequences and a sequence encoding a signal peptide leader directing transport of the downstream fusion 20 21 protein to the periplasmic space. The library of unknown light chains (VL and CL) is expressed 22 separately from a phagemid expression vector which also 23 contains the oestrogen receptor HRE sequence. Thus when 24 both heavy and light chains are expressed in the same 25 host cell, following infection with the phage 26 containing the heavy chain-DBD fusion, the light chain 27 phagemid vector is preferentially packaged into mature 28 phage particles as single stranded DNA, which is bound 29 by the heavy chain-DBD fusion protein during the 30 packaging process. The light chain proteins are 31 transported to the periplasm where they assemble with 32 the heavy chain that is fused to the DBD protein as it 33 exits the cell on the PDCP. In this example the DBD 34 35 fusion protein and the HRE DNA sequences are not encoded on the same vector, the unknown peptide 36

- sequences are present on the same vector as the HRE
- 2 sequence. Peptide display carrier packages (PDCP) which
- 3 encode the protein of interest can then be selected by
- 4 means of a ligand specific for the antibody.

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Table 1 Committee (18 Care 19 All Care

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Table 1 (i) Oligonucleotide primers used for human scFv library construction

CDNA synthesis primers

| IGMCDNAFOR | TGGAAGAGGCACGTTCTTTCTTT |
|------------|-----------------------------|
| IgDCDNAFOR | CTCCTTCTTACTCTTGCTGGCGGT |
| IgKCDNAFOR | AGACTCTCCCCTGTTGAAGCTCTT |
| IgACDNAFOR | TGAAGATTCTGTAGGGGCCACTGTCTT |

JHFOR primers

| JH1-2FOR | TGAACCGCCTCCACCTGAGGAGACGGTGACCAGGGTGCC |
|----------|---|
| JH3FOR | TGAACCGCCTCCACCTGAAGAGACGGTGACCATTGTCCC |
| JH4-5FOR | TGAACCGCCTCCACCTGAGGAGACGGTGACCAGGGTTCC |
| JH6FOR | TGAACCGCCTCCACCTGAGGAGACGGTGACCGTGGTCCC |

VH familyBAKprimers

| VH1BAK | TTTTTGGCCCAGCCGGCCATGGCCCAGGTGCAGCTGGTGCAGTCTGG |
|--------|---|
| VH2BAK | TTTTTGGCCCAGCCGGCCATGGCCCAGGTCAACTTAAGGGAGTCTGG |
| VH3BAK | TTTTTGGCCCAGCCGGCCATGGCCGAGGTGCAGCTGGTGGAGTCTGG |
| VH4BAK | TTTTTGGCCCAGCCGGCCATGGCCCAGGTGCAGCTGCAGGAGTCGGG |
| VH5BAK | TTTTTGGCCCAGCCGCCATGGCCGAGGTGCAGCTGTTGCAGTCTGC |
| VH6BAK | TTTTTGGCCCAGCCGCCATGGCCCAGGTACAGCTGCAGCAGTCAGG |
| | |

Light chain FOR primers

| SCFVKFOR | TTATTCGCGGCCGCCTAAACAGAGGCAGTTCCAGATTTC. |
|----------|--|
| SCFVAFOR | GTCACTTGCGGCCGCCTACAGTGTGGCCTTGTTGGCTTG. |

VK family BAK primers

| VK1BAK | TCTGGCGGTGGCGGATCGGACATCCAGATGACCCAGTCTCC |
|--------|---|
| VK2BAK | TCTGGCGGTGGCGGATCGGATGTTGTGATGACTCAGTCTCC |
| VK3BAK | TCTGGCGGTGGCGGATCGGAAATTGTGTTGACGCAGTCTCC |
| VK4BAK | TCTGGCGGTGGCGATCGGACATCGTGATGACCCAGTCTCC |
| VK5BAK | TCTGGCGGTGGCGGATCGGAAACGACACTCACGCAGTCTCC |
| VK6BAK | TCTGGCGGTGGCGGATCGGAAATTGTGCTGACTCAGTCTCC |

JK FOR primers

| JK1FOR | TTCTCGTGCGGCCGCCTAACGTTTGATTTCCACCTTGGTCCC |
|---------------|--|
| JK2FOR | TTCTCGTGCGGCCGCCTAACGTTTGATCTCCAGCTTGGTCCC |
| JK3FOR | TTCTCGTGCGGCCGCCTAACGTTTGATATCCACTTTGGTCCC |
| JK4FOR | TTCTCGTGCGGCCGCCTAACGTTTGATCTCCACCTTGGTCCC |
| JK5FOR | TTCTCGTGCGGCCGCCTAACGTTTAATCTCCAGTCGTGTCCC |

VA family BAK primers

| Vλ1BAK | TCTGGCGGTGGCGGATCGCAGTCTGTGTTGACGCAGCCGCC |
|--------|---|
| Vλ2BAK | TCTGGCGGTGGCGGATCGCAGTCTGCCCTGACTCAGCCTGC |

Table 1 (ii) Oligonucleotide primers used for human scFv library construction

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| VA3aBAK | TCTGGCGGTGGCGATCGTCCTATGTGCTGACTCAGCCACC |
|-----------------|---|
| V λ3bBAK | TCTGGCGGTGGCGGATCGTCTTCTGAGCTGACTCAGGACCC |
| Vλ4BAK | TCTGGCGGTGGCGGATCGCACGTTATACTGACTCAACCGCC |
| Vλ5BAK | TCTGGCGGTGGCGGATCGCAGGCTGTGCTCACTCAGCCGTC |
| Vλ6BAK | TCTGGCGGTGGCGGATCGAATTTTATGCTGACTCAGCCCCA |
| | 大学的时间,这是一个人,这些大人的发展,这个大人的对象的,就是这种人的人的人的人的人的人的人,也是这个人的人。 |

J_{\(\right)} primers

| JλlFOR | TTCTCGTGCGGCCGCCTAACCTAGGACGGTGACCTTGGTGCC |
|----------|--|
| JA2-3FOR | TTCTCGTGCGGCCGCCTAACCTAGGACGGTCAGCTTGGTCCC |
| Jλ4-5FOR | TTCTCGTGCGGCCGCCTAACCTAAAACGGTGAGCTGGGTCCC |

Linker primers

| LINKAMP3 | CGATCCGCCACGCCAGA |
|-----------|---|
| LINKAMP5 | GTCTCCTCAGGTGGAGGC |
| LINKAMP3T | CGATCCGCCACGCCAGAGCCACCTCCGCCTGAACCGCCTCCACCTGAGGAGAC |

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